

GenCore version 4.5
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om protein - protein search, using sw model

Run on: March 12, 2002, 12:54:21 : Search time 45.9 seconds
(without alignments)
40,744 million cell updates/sec

Title: US-09-801-784-36
Perfect score: 50
Sequence: 1 PSAVALTYSIP 10

Scoring table: BLAST/MS62
Gapop 10.0, Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Minimum number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0.8
Listing first 45 summaries

Database :

SPTREMBL_17: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_oropharynx: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	84.0	134	2	047122
2	40	80.0	433	1	09DE24
3	38	76.0	114	12	041238
4	38	76.0	114	12	041239
5	38	76.0	114	12	041240
6	38	76.0	114	12	041241
7	38	76.0	159	12	09YR11
8	38	76.0	233	12	091P02
9	38	76.0	270	5	09NE74
10	38	76.0	579	12	086124
11	38	76.0	579	12	09WJ53
12	38	76.0	695	12	086123
13	38	76.0	2344	12	086117
14	38	76.0	2344	12	086119
15	37	74.0	534	2	09ANK2
16	36	72.0	114	12	041209
17	36	72.0	114	12	041210
18	36	72.0	114	12	041211
19	36	72.0	114	12	041212

20	36	72.0	114	12	041213
21	36	72.0	114	12	041214
22	36	72.0	114	12	041215
23	36	72.0	114	12	041218
24	36	72.0	114	12	041219
25	36	72.0	114	12	041220
26	36	72.0	114	12	041221
27	36	72.0	114	12	041222
28	36	72.0	114	12	041223
29	36	72.0	114	12	041226
30	36	72.0	114	12	041229
31	36	72.0	114	12	041231
32	36	72.0	114	12	041232
33	36	72.0	114	12	041234
34	36	72.0	114	12	041237
35	36	72.0	114	12	041242
36	36	72.0	255	2	092A13
37	36	72.0	255	2	091P03
38	36	72.0	342	2	099Y46
39	36	72.0	427	3	074498
40	36	72.0	537	3	002466
41	36	72.0	579	12	09YND3
42	36	72.0	579	12	091208
43	36	72.0	2344	12	086114
44	36	72.0	114	12	041216
45	36	70.0	114	12	041217

ALIGNMENTS

RESULT 1	047122	PRELIMINARY:	PRT:	134 AA.
AC	047122:			
PE	01-NOV-1996 (LIFEMBL01_01, created)			
DE	01-NOV-1996 (LIFEMBL01_01, last sequence update)			
PI	01-AUG-1998 (LIFEMBL01_07, last annotation update)			
DE	CSFA PROTEIN (PROMOTED).			
GN	CSFA.			
OS	Escherichia coli.			
OC	Bacteriophagocytosis; gamma subdivision; Enterobacteriaceae.			
OX	Escherichia.			
OX	Metab. Taxid 562:			
KN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-961373:			
RA	Gaestira W., Kusters J.G., Van Dijk L.			
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: X97494; CAA66124.1; .			
FT	NON_TER			
FT	NON_TER			
FT	NON_TER			
SEQ	SEQUENCE	134 AA:	13016 MW:	488953861966A (7694):
Query Match	84.0%:	Score 42:	DB 2:	Length 134:
Best Local Similarity	80.0%:	Pred. No. 13:		
Matches	8: conservative	1: mismatches	1: indels	0: gaps
QY	1 PSAVALTYSIP 10			
DB	11111111			
DB	16 PTAVALTYSIP 25			
RESULT 2	09DE24	PRELIMINARY:	PRT:	433 AA.
AC	09DE24:			
PE	01-MAR-2001 (LIFEMBL01_16, created)			
DE	01-MAR-2001 (LIFEMBL01_16, last sequence update)			
PI	01-JUN-2001 (LIFEMBL01_17, last annotation update)			
DE	PROKHA: TRANSLOCATION FACTOR CL 2.			
GN	FOXC1.2.			

№ 181_1ax11a_5664;

[illegible]

108	InterPro: IPR016445; Calico coat
109	Pfam: PF07979; Calico coat 1.
110	SEQUENCE 579 AA; 60195 MW; D806D11A06ZL6AA CDS; 4
111	
Query Match:	76.0%; Score 48; DB 12; Length 579;
Best Local Similarity	70.0%; Pred. No. 45;
Matches	7; Conserved 2; Missed 0; Indels 0; Gaps 0;
DJ	1 PSANALYSP 10
DB	429 PSANALYSP 438
RESULT 12	
CDS	PRELIMINARY: PKT: 579 AA.
CDSDS	
DT	01-NOV-1999 (EMBL) : 12; (Genbank)
DT	01-NOV-1999 (EMBL) : 12; last sequence update)
DT	01-JUN-2001 (EMBL) : 17; last annotation update)
DE	CAVSH1 STRUTHERAL PROTEIN VP60.
GN	VP60.
OS	Rabbit haemorrhagic disease virus (RHDV).
OR	Virusus; SSRNA positive strand viruses; no DNA stage; Caliciviridae;
OX	Lacovirus.
OX	NCH Loxlo 11976;
GN	(1)
KI	SEQUENCE FROM N.A.
RC	SIRKEN EISENHEDTENSTAMP;
RA	Schottmeyer H., Reinhardt T., Kuehlhorst B.;
RT	"Molecular, antigenic and molecular properties of rabbit haemorrhagic
RI	disease virus (RHDV) isolated from vaccinated rabbits: detection and
RL	preliminary characterization of antigenic variants.";
RR	Submitted (Nov 1997) to the EMBL/Genbank/DDBJ databases.
RR	EMBL: Y15440; GenBank: F5641.1;
DR	InterPro: IPRO15443; RefSeq: NC_011111.1;
DR	Pfam: PF09915; Calico coat 1.
SR	SEQUENCE 579 AA; 60262 MW; 7264E5EF1B06280B CDS; 4
112	
Query Match:	76.0%; Score 48; DB 12; Length 579;
Best Local Similarity	70.0%; Pred. No. 45;
Matches	7; Conserved 2; Missed 0; Indels 0; Gaps 0;
DJ	1 PSANALYSP 10
DB	429 PSANALYSP 438
RESULT 12	
CDS	PRELIMINARY: PKT: 579 AA.
CDSDS	
DT	01-NOV-1999 (EMBL) : 01; (Genbank)
DT	01-NOV-1999 (EMBL) : 01; last sequence update)
DT	01-JUN-2001 (EMBL) : 17; last annotation update)
DE	CAVSH1 STRUTHERAL PROTEIN VP60.
GN	VP60.
OS	Rabbit haemorrhagic disease virus (RHDV).
OR	Virusus; SSRNA positive strand viruses; no DNA stage; Caliciviridae;
OX	Lacovirus.
OX	NCH Loxlo 11976;
GN	(1)
KI	SEQUENCE FROM N.A.
RC	SIRKEN AS1/89;
RA	MELINE WSGA/42; Pollock RD7041;
RA	Boud J., Cassals R., Martin M., Martin Alonso J., Carnaudes P.,
RA	Frieto M., Paria F.;
RI	"Molecular cloning, sequencing and expression in Escherichia coli of
RI	the capsid protein gene from rabbit haemorrhagic disease virus
RI	(Spanish isolate ASI/89).";
RI	J. Gen. Virol. 75(2409-2414 (1994).
GN	(2)

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RP SEQUENCE FROM N.A.
RC STRAIN AST/89;
RX MEDLINE=94070565; PubMed 1441746;
RA Bosa J., Martin M., Casals R., Prieto M., Parra F.:
RT "In vitro translation of a subgenomic mRNA from purified variants of
RL the Spanish field isolate AST/89 of rabbit hemorrhagic disease virus
RM (RHDV).";
RN Virus Res. 26:33-40(1992).
RP SEQUENCE OF 1-149 FROM N.A.
RC STRAIN-AST/89;
RX MEDLINE=94255896; PubMed 8488721;
RA Parra F., Bosa J.A., Martin M.S., Casals R.:
RT "The amino terminal sequence of VP60 from rabbit hemorrhagic disease
RM virus supports its putative subgenomic origin.";
RN Virus Res. 27:219-228(1993).
RP SEQUENCE FROM N.A.
RC STRAIN-AST/89;
RA Parra F.:
RT Submitted (JUL-1993) to the EMBL/GenBank/DBJ databases.
RM EMBL: Z24757; CAA80881.1;
RN InterPro: IPR001643; Calicl_coat;
RX Pfam: PF00915; Calicl_coat; 1;
DR PRINTS: PR00918; CALICIVIRUSNS.
FT NUNTER 1
SO SEQUENCE 695 AA: 73731 MW: 620921628969898A Cleaved;

Query Match 76.0%; Score 48; DB 12; Length 244;
Best Local Similarity 70.0%; Pred. No. 1; 5e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

UY 1 PSANALTYSP 10
Db 545 PSANALTYSP 554

RESULT 13
Q06117 PRELIMINARY; PRT: 244 AA.
ID Q06117;
AC Q06117;
DE 01-NOV-1996 (TREMURel. 01, created)
DT 01-NOV-1996 (TREMURel. 01, last sequence update)
DT 01-JUN-2001 (TREMURel. 17, last annotation update)
DE (SD):
OS Rabbit hemorrhagic disease virus (RHDV).
OC Viruses; ssRNA positive-strand viruses, no RNA stage; Caliciviridae;
OC Lagovirus.
NCBI_TaxID=11976;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN-SD;
RX MEDLINE=95250304; PubMed-7732658;
RA Rasseghieri D., Huguet S., Madelaine M.F., Vautherot J.F.:
RT "Sequence and genomic organization of a rabbit hemorrhagic disease
RM virus isolated from a wild rabbit.";
RN Virus Genes 9:121-132(1995).
DE EMBL: Z29514; CAA82635.1;
RN InterPro: IPR000317; Endoplase_C24;
DR InterPro: IPR000605; RNA_helicase;
DR InterPro: IPR001205; RNA_pol_P4D;
DR InterPro: IPR001643; Calicl_coat;
DR Pfam: PF00680; RNA_dep_RNA_pol; 1;
DR Pfam: PF00910; RNA_dep_RNA_pol; 1;
DR Pfam: PF00915; Calicl_coat; 1;
DR PRINTS: PR00916; ZCENDOPVASE;
DR PRINTS: PR00918; CALICIVIRUSNS.
SO SEQUENCE 244 AA: 257120 MW: 194013447558877 Cleaved;

Query Match 76.0%; Score 48; DB 12; Length 244;
Best Local Similarity 70.0%; Pred. No. 1; 5e+02;

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Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

UY 1 PSANALTYSP 10
Db 2194 PSANALTYSP 2203

RESULT 14
Q06117 PRELIMINARY; PRT: 244 AA.
ID Q06117;
AC Q06117;
DE 01-NOV-1996 (TREMURel. 01, created)
DT 01-NOV-1996 (TREMURel. 01, last sequence update)
DT 01-JUN-2001 (TREMURel. 17, last annotation update)
DE (SD):
OS Rabbit hemorrhagic disease virus (RHDV).
OC Viruses; ssRNA positive-strand viruses, no RNA stage; Caliciviridae;
OC Lagovirus.
NCBI_TaxID=11976;
RN 11;
RP SEQUENCE OF 149-244 FROM N.A.
RC STRAIN-AST/89;
RX MEDLINE=94458742; PubMed 8077941;
RA Bosa J., Casals R., Martin M., Prieto M., Alonso J., Calmeiros R.:
RT "Molecular cloning, sequencing and expression in Escherichia coli of
RM the capsid protein gene from rabbit hemorrhagic disease virus
RL (Spanish isolate AST/89).";
RN J. Gen. Virol. 75:2409-2413(1994).
RP SEQUENCE OF 149-1795 FROM N.A.
RC STRAIN-AST/89;
RX MEDLINE=94255896; PubMed 8488721;
RA Parra F., Bosa J.A., Martin M.S., Casals R.:
RT "The amino terminal sequence of VP60 from rabbit hemorrhagic disease
RM virus supports its putative subgenomic origin.";
RN Virus Res. 27:219-228(1993).
RN 13;
RP SEQUENCE FROM N.A.
RC STRAIN-AST/89;
RA Casals R., Martin Alonso J., Bosa J., Parra F.:
RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RM EMBL: Z49271; CAA89265.1;
RN InterPro: IPR00317; Endoplase_C24;
DR InterPro: IPR006005; RNA_helicase;
DR InterPro: IPR001205; RNA_pol_P4D;
DR InterPro: IPR001643; Calicl_coat; 1;
DR Pfam: PF00680; RNA_dep_RNA_pol; 1;
DR Pfam: PF00910; RNA_dep_RNA_pol; 1;
DR Pfam: PF00915; Calicl_coat; 1;
DR PRINTS: PR00916; ZCENDOPVASE;
DR PRINTS: PR00918; CALICIVIRUSNS.
KM Polyprotein;
SO SEQUENCE 244 AA: 256769 MW: 92640696649964 Cleaved;

Query Match 76.0%; Score 48; DB 12; Length 244;
Best Local Similarity 70.0%; Pred. No. 1; 5e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

UY 1 PSANALTYSP 10
Db 2194 PSANALTYSP 2203

RESULT 15
Q06117 PRELIMINARY; PRT: 544 AA.
ID Q06117;
AC Q06117;
DE 01-JUN-2001 (TREMURel. 17, created)
DT 01-JUN-2001 (TREMURel. 17, last sequence update)
DT 01-JUN-2001 (TREMURel. 17, last annotation update)

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